RAW SEQUENCE LISTING

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Application Serial Number: _10764,260_
Source: _IFW_
Date Processed by STIC: _1-3-05_

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IFWO

RAW SEQUENCE LISTING   DATE: 01/03/2005
PATENT APPLICATION: US/10/764,260   TIME: 15:40:27

Input Set : A:\54318.8009.US01.txt
Output Set: N:\CRF4\01032005\J764260.raw

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 3 <110> APPLICANT: Debe, Derek A.
 4         Danzer, Joseph F.
 5         Xie, Lei
 7 <120> TITLE OF INVENTION: METHOD FOR DETERMINING FUNCTIONAL SITES IN A PROTEIN
 9 <130> FILE REFERENCE: 54318.8009.US01
11 <140> CURRENT APPLICATION NUMBER: US 10/764,260
12 <141> CURRENT FILING DATE: 2004-01-22
14 <150> PRIOR APPLICATION NUMBER: US 60/447,562
15 <151> PRIOR FILING DATE: 2003-02-14
17 <160> NUMBER OF SEQ ID NOS: 29
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 327
23 <212> TYPE: PRT
24 <213> ORGANISM: Escherichia coli
26 <400> SEQUENCE: 1
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32 Ser Arg Gln Leu Glu Glu Arg Leu Gly Leu Ile Glu Val Gln Ala Pro
33                 20                  25                  30
36 Ile Leu Ser Arg Val Gly Asp Gly Thr Gln Asp Asn Leu Ser Gly Ala
37             35                  40                  45
40 Glu Lys Ala Val Gln Val Lys Val Lys Ala Leu Pro Asp Ala Gln Phe
41     50                  55                  60
44 Glu Val Val His Ser Leu Ala Lys Trp Lys Arg Gln Thr Leu Gly Gln
45 65                  70                  75                  80
48 His Asp Phe Ser Ala Gly Glu Gly Leu Tyr Thr His Met Lys Ala Leu
49                 85                  90                  95
52 Arg Pro Asp Glu Asp Arg Leu Ser Pro Leu His Ser Val Tyr Val Asp
53                 100                 105                 110
56 Gln Trp Asp Trp Glu Arg Val Met Gly Asp Gly Glu Arg Gln Phe Ser
57             115                 120                 125
60 Thr Leu Lys Ser Thr Val Glu Ala Ile Trp Ala Gly Ile Lys Ala Thr
61     130                 135                 140
64 Glu Ala Ala Val Ser Glu Glu Phe Gly Leu Ala Pro Phe Leu Pro Asp
65 145                 150                 155                 160
68 Gln Ile His Phe Val His Ser Gln Glu Leu Leu Ser Arg Tyr Pro Asp
69                 165                 170                 175
72 Leu Asp Ala Lys Gly Arg Glu Arg Ala Ile Ala Lys Asp Leu Gly Ala
73             180                 185                 190
76 Val Phe Leu Val Gly Ile Gly Gly Lys Leu Ser Asp Gly His Arg His
77             195                 200                 205
80 Asp Val Arg Ala Pro Asp Tyr Asp Asp Trp Ser Thr Pro Ser Glu Leu
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84  Gly His Ala Gly Leu Asn Gly Asp Ile Leu Val Trp Asn Pro Val Leu
85  225                 230                 235                 240
88  Glu Asp Ala Phe Glu Leu Ser Ser Met Gly Ile Arg Val Asp Ala Asp
89                  245                 250                 255
92  Thr Leu Lys His Gln Leu Ala Leu Thr Gly Asp Glu Asp Arg Leu Glu
93                  260                 265                 270
96  Leu Glu Trp His Gln Ala Leu Leu Arg Gly Glu Met Pro Gln Thr Ile
97              275                 280                 285
100 Gly Gly Gly Ile Gly Gln Ser Arg Leu Thr Met Leu Leu Leu Gln Leu
101         290                 295                 300
104 Pro His Ile Gly Gln Val Gln Ala Gly Val Trp Pro Ala Ala Val Arg
105 305                 310                 315                 320
108 Glu Ser Val Pro Ser Leu Leu
109                 325
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 327
114 <212> TYPE: PRT
115 <213> ORGANISM: Shigella flexneri
117 <400> SEQUENCE: 2
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123 Ser Arg Gln Leu Glu Glu Arg Leu Gly Leu Ile Glu Val Gln Ala Pro
124             20                  25                  30
127 Ile Leu Ser Arg Val Gly Asp Gly Thr Gln Asp Asn Leu Ser Gly Cys
128         35                  40                  45
131 Glu Lys Ala Val Gln Val Lys Val Lys Ala Leu Pro Asp Ala Gln Phe
132     50                  55                  60
135 Glu Val Val His Ser Leu Ala Lys Trp Lys Arg Gln Thr Leu Gly Gln
136 65                  70                  75                  80
139 His Asp Phe Ser Ala Gly Glu Gly Leu Tyr Thr His Met Lys Ala Leu
140                 85                  90                  95
143 Arg Pro Asp Glu Asp Arg Leu Ser Pro Leu His Ser Val Tyr Val Asp
144             100                 105                 110
147 Gln Trp Asp Trp Glu Arg Val Met Gly Asp Gly Glu Arg Gln Leu Ser
148         115                 120                 125
151 Thr Leu Lys Ser Thr Val Glu Ala Ile Trp Ala Gly Ile Lys Ala Thr
152     130                 135                 140
155 Glu Ala Ala Val Asn Glu Glu Phe Gly Leu Ala Pro Phe Leu Pro Asp
156 145                 150                 155                 160
159 Gln Ile His Phe Val His Ser Gln Glu Leu Leu Ser Arg Tyr Pro Asp
160             165                 170                 175
163 Leu Asp Ala Lys Gly Arg Glu Arg Ala Ile Ala Lys Asp Leu Gly Ala
164             180                 185                 190
167 Val Phe Leu Val Gly Ile Gly Gly Lys Leu Ser Asp Gly His Arg His
168         195                 200                 205
171 Asp Val Arg Ala Pro Asp Tyr Asp Asp Trp Ser Thr Pro Ser Glu Leu
172     210                 215                 220
175 Gly His Ala Gly Leu Asn Gly Asp Ile Leu Val Trp Asn Pro Val Leu
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Input Set : A:\54318.8009.US01.txt
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176 225                      230                   235                     240
179 Glu Asp Ala Phe Glu Leu Ser Ser Met Gly Ile Arg Val Asp Ala Asp
180                     245                   250                   255
183 Thr Leu Lys His Gln Leu Ala Leu Thr Gly Asp Glu Asp Arg Leu Gln
184                     260                   265                   270
187 Leu Glu Trp His Gln Ala Leu Leu Arg Gly Glu Met Pro Gln Thr Ile
188               275                   280                   285
191 Gly Gly Gly Ile Gly Gln Ser Arg Leu Thr Met Leu Leu Leu Gln Leu
192         290                   295                   300
195 Pro His Ile Gly Gln Val Gln Cys Gly Val Trp Pro Ala Ala Val Arg
196 305                      310                   315                     320
199 Glu Ser Val Pro Ser Leu Leu
200                     325
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204 <211> LENGTH: 327
205 <212> TYPE: PRT
206 <213> ORGANISM: Salmonella enterica
208 <400> SEQUENCE: 3
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214 Ser Arg Gln Leu Glu Glu Arg Leu Gly Leu Ile Glu Val Gln Ala Pro
215                     20                   25                    30
218 Ile Leu Ser Arg Val Gly Asp Gly Thr Gln Asp Asn Leu Ser Gly Cys
219               35                   40                   45
222 Glu Lys Ala Val Gln Val Lys Val Lys Ala Leu Pro Asp Ala Gln Phe
223         50                        55                   60
226 Glu Val Val His Ser Leu Ala Lys Trp Lys Arg Gln Thr Leu Gly Gln
227 65                      70                   75                        80
230 His Asp Phe Ser Ala Gly Glu Gly Leu Tyr Thr His Met Lys Ala Leu
231                     85                   90                    95
234 Arg Pro Asp Glu Asp Arg Leu Ser Pro Leu His Ser Val Tyr Val Asp
235                     100                  105                  110
238 Gln Trp Asp Trp Glu Arg Val Met Gly Asp Gly Glu Arg Gln Phe Ser
239         115                  120                   125
242 Thr Leu Lys Ser Thr Val Glu Ala Ile Trp Ala Gly Ile Lys Ala Thr
243         130                  135                  140
246 Glu Ala Glu Val His Lys Gln Phe Gly Leu Ala Pro Phe Leu Pro Asp
247 145                     150                  155                       160
250 Gln Ile His Phe Val His Ser Gln Glu Leu Leu Ala Arg Phe Pro Asp
251                     165                  170                  175
254 Leu Asp Ala Lys Gly Arg Glu Arg Ala Ile Ala Lys Glu Leu Gly Ala
255               180                  185                  190
258 Val Phe Leu Val Gly Ile Gly Gly Lys Leu Ser Asp Gly Arg Arg His
259         195                  200                   205
262 Asp Val Arg Ala Pro Asp Tyr Asp Asp Trp Ser Ser Ala Ser Glu Leu
263         210                  215                   220
266 Gly Tyr Ala Gly Leu Asn Gly Asp Ile Leu Val Trp Asn Pro Val Leu
267 225                     230                  235                     240
270 Glu Asp Ala Phe Glu Leu Ser Ser Met Gly Ile Arg Val Asp Ala Asp
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Input Set : A:\54318.8009.US01.txt
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271                 245               250               255
274 Thr Leu Met Arg Gln Leu Ala Leu Thr Gly Asp Glu Asp Arg Leu Gln
275                 260                 265               270
278 Leu Glu Trp His Gln Ala Leu Leu Arg Gly Glu Met Pro Gln Thr Ile
279             275                 280                 285
282 Gly Gly Gly Ile Gly Gln Ser Arg Leu Thr Met Leu Leu Leu Gln Leu
283         290                 295                 300
286 Pro His Ile Gly Gln Val Gln Cys Gly Val Trp Pro Ala Gln Val Arg
287 305                 310                 315                 320
290 Glu Ser Ile Pro Ala Ile Leu
291                 325
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 327
296 <212> TYPE: PRT
297 <213> ORGANISM: Salmonella typhimurium
299 <400> SEQUENCE: 4
301 Ala Tyr Ile Ala Lys Gln Arg Gln Ile Ser Phe Val Lys Ser His Phe
302 1               5                   10                15
305 Ser Arg Gln Leu Glu Glu Arg Leu Gly Leu Ile Glu Val Gln Ala Pro
306                 20                  25                30
309 Ile Leu Ser Arg Val Gly Asp Gly Thr Gln Asp Asn Leu Ser Gly Cys
310             35                  40                  45
313 Glu Lys Ala Val Gln Val Lys Val Lys Ala Leu Pro Asp Ala Gln Phe
314         50                  55                  60
317 Glu Val Val His Ser Leu Ala Lys Trp Lys Arg Gln Thr Leu Gly Gln
318 65                  70                  75                80
321 His Asp Phe Ser Ala Gly Glu Gly Leu Tyr Thr His Met Lys Ala Leu
322             85                  90                  95
325 Arg Pro Asp Glu Asp Arg Leu Ser Pro Leu His Ser Val Tyr Val Asp
326                 100                 105               110
329 Gln Trp Asp Trp Glu Arg Val Met Gly Asp Gly Glu Arg Gln Phe Ser
330             115                 120                 125
333 Thr Leu Lys Ser Thr Val Glu Ala Ile Trp Ala Gly Ile Lys Ala Thr
334         130                 135                 140
337 Glu Ala Glu Val His Lys Gln Phe Gly Leu Ala Pro Phe Leu Pro Glu
338 145                 150                 155               160
341 Gln Ile Gln Phe Val His Ser Gln Glu Leu Leu Ala Arg Phe Pro Asp
342             165                 170                 175
345 Leu Asp Ala Lys Gly Arg Glu Arg Ala Ile Ala Lys Glu Leu Gly Ala
346             180                 185                 190
349 Val Phe Leu Val Gly Ile Gly Gly Lys Leu Ser Asp Gly His Arg His
350             195                 200                 205
353 Asp Val Arg Ala Pro Asp Tyr Asp Asp Trp Ser Ser Ala Ser Glu Leu
354         210                 215                 220
357 Gly Tyr Ala Gly Leu Asn Gly Asp Ile Leu Val Trp Asn Pro Val Leu
358 225                 230                 235               240
361 Glu Asp Ala Phe Glu Leu Ser Ser Met Gly Ile Arg Val Asp Ala Asp
362             245                 250                 255
365 Thr Leu Met Arg Gln Leu Ala Leu Thr Gly Asp Glu Asp Arg Leu Gln
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Input Set : A:\54318.8009.US01.txt
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366              260              265              270
369 Leu Glu Trp His Gln Ala Leu Leu Arg Gly Glu Met Pro Gln Thr Ile
370          275              280              285
373 Gly Gly Gly Ile Gly Gln Ser Arg Leu Thr Met Leu Leu Leu Gln Leu
374      290              295              300
377 Pro His Ile Gly Gln Val Gln Cys Gly Val Trp Pro Ala Gln Val Arg
378 305              310              315                  320
381 Glu Ser Ile Pro Ala Ile Leu
382              325
385 <210> SEQ ID NO: 5
386 <211> LENGTH: 327
387 <212> TYPE: PRT
388 <213> ORGANISM: Yersinia pestis
390 <400> SEQUENCE: 5
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393 1              5              10               15
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397              20               25               30
400 Ile Leu Ser Arg Val Gly Asp Gly Thr Gln Asp Asn Leu Ser Gly Ser
401          35               40               45
404 Glu Lys Ala Val Gln Val Lys Val Lys Ser Leu Pro Asp Ser Thr Phe
405      50               55               60
408 Glu Val Val His Ser Leu Ala Lys Trp Lys Arg Lys Thr Leu Gly Arg
409 65               70               75                  80
412 Phe Asp Phe Gly Ala Asp Gln Gly Val Tyr Thr His Met Lys Ala Leu
413              85               90               95
416 Arg Pro Asp Glu Asp Arg Leu Ser Ala Ile His Ser Val Tyr Val Asp
417              100              105              110
420 Gln Trp Asp Trp Glu Arg Val Met Gly Asp Gly Glu Arg Asn Leu Ala
421          115              120              125
424 Tyr Leu Lys Ser Thr Val Asn Lys Ile Tyr Ala Ala Ile Lys Glu Thr
425      130              135              140
428 Glu Ala Ala Ile Ser Ala Glu Phe Gly Val Lys Pro Phe Leu Pro Asp
429 145              150              155              160
432 His Ile Gln Phe Ile His Ser Glu Ser Leu Arg Ala Arg Phe Pro Asp
433              165              170              175
436 Leu Asp Ala Lys Gly Arg Glu Arg Ala Ile Ala Lys Glu Leu Gly Ala
437              180              185              190
440 Val Phe Leu Ile Gly Ile Gly Gly Lys Leu Ala Asp Gly Gln Ser His
441          195              200              205
444 Asp Val Arg Ala Pro Asp Tyr Asp Asp Trp Thr Ser Pro Ser Ala Glu
445      210              215              220
448 Gly Phe Ser Gly Leu Asn Gly Asp Ile Ile Val Trp Asn Pro Ile Leu
449 225              230              235              240
452 Glu Asp Ala Phe Glu Ile Ser Ser Met Gly Ile Arg Val Asp Ala Glu
453              245              250              255
456 Ala Leu Lys Arg Gln Leu Ala Leu Thr Gly Asp Glu Asp Arg Leu Glu
457              260              265              270
460 Leu Glu Trp His Gln Ser Leu Leu Arg Gly Glu Met Pro Gln Thr Ile
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VERIFICATION SUMMARY   DATE: 01/03/2005
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Output Set: N:\CRF4\01032005\J764260.raw